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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: Fri Sep 21 11:50:38 EDT 2007

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Application No: 10579936 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-12 14:58:22.381
Finished: 2007-09-12 14:58:23.791
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 410 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 47
Actual SeqID Count: 47

Error code	Error Description
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SEQUENCE LISTING

<110> TAKEDA, Junji
HORIE, Kyoji
YUSA, Kosuke
ISHIHARA, Hiroshi

<120> DEVELOPMENT OF MAMMALIAN GENOME MODIFICATION TECHNIQUE
USING RETROTRANSPOSON

<130> 710048.401USPC

<140> 10579936
<141> 2007-09-12

<150> PCT/JP2004/017307
<151> 2004-11-19

<150> JP 2003-393175
<151> 2003-11-21

<160> 47

<170> PatentIn version 3.2

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actcatcagc tggggAACGA CGGTGATAAA GGTTCCCGTA AAGCAGACTG TAAAAAAGGA	660
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Met Asn Ser Glu Leu Phe Ser Trp Gly Thr Arg Val Pro Val	
1 5 10	
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Ser Met Phe Gly Leu Glu Phe Phe Leu Val Leu Gly Ala Leu Leu Phe	
15 20 25 30	
ctt ttc aca tgt tat ata gtg gtt aag gca ggg ctg aaa att ctg gat	807
Leu Phe Thr Cys Tyr Ile Val Val Lys Ala Gly Leu Lys Ile Leu Asp	
35 40 45	
gaa att cag ggc agt cta tca gaa gta aag cgg gga gag aga gta gga	855
Glu Ile Gln Gly Ser Leu Ser Glu Val Lys Arg Gly Glu Arg Val Gly	
50 55 60	
gca agg aga aac ggt aag tat aca ggc ctt tcc aag ggt ctt gaa ccc	903
Ala Arg Arg Asn Gly Lys Tyr Thr Gly Leu Ser Lys Gly Leu Glu Pro	
65 70 75	
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Glu Glu Lys Leu Arg Leu Gly Arg Asn Thr Trp Arg Glu Ile Arg Arg	
80 85 90	
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Lys Arg Gly Lys Arg Glu Lys Lys Asp Arg Leu Ala Glu Val Ser	
95 100 105 110	
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Arg Arg Tyr Ser Ser Leu Asp Glu Leu Arg Lys Pro Ala Leu Ser Ser	
115 120 125	
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Ser Glu Ala Ser Glu Glu Ser Ser Glu Glu Thr Asp Trp Glu Glu	
130 135 140	
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Glu Ala Ala His Tyr Gln Pro Ala Asn Trp Ser Arg Lys Lys Pro Lys	
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Ala Ala Gly Glu Ser Gln Arg Thr Val Gln Pro Pro Gly Ser Arg Phe	
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Gln Gly Pro Pro Tyr Ala Glu Pro Pro Cys Val Val Arg Gln Gln	
175 180 185 190	
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Cys Ala Glu Arg Gln Cys Ala Glu Arg Cys Ala Glu Arg Gln Cys Ala	
195 200 205	
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Asp Arg Cys Ala Glu Arg Gln Cys Ala Glu Arg Gln Cys Ala Asp Ser	
210 215 220	

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Phe Ile Pro Arg Glu Glu Gln Lys Lys Ile Glu Gln Ala Phe Pro Val			
225	230	235	
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Phe Glu Gly Ala Glu Gly Gly Arg Val His Ala Pro Val Glu Tyr Val			
240	245	250	
cag att aag gaa att gcc gag tcg gtt cgt aaa tac gga acc aat gct			1479
Gln Ile Lys Glu Ile Ala Glu Ser Val Arg Lys Tyr Gly Thr Asn Ala			
255	260	265	270
aat ttc acc ttg gtg cag tta gac agg ctc gct ggt atg gca cta acg			1527
Asn Phe Thr Leu Val Gln Leu Asp Arg Leu Ala Gly Met Ala Leu Thr			
275	280	285	
cct gct gat tgg cag acg gtt gta aaa gcc gct ctt cct agt atg ggc			1575
Pro Ala Asp Trp Gln Thr Val Val Lys Ala Ala Leu Pro Ser Met Gly			
290	295	300	
aaa tat atg gaa tgg aaa gcg ctt tgg cac gaa gct gca cag gcg cag			1623
Lys Tyr Met Glu Trp Lys Ala Leu Trp His Glu Ala Ala Gln Ala Gln			
305	310	315	
gcc cga gca aac gca gct gct ttg act cca gag cag aga gat tgg act			1671
Ala Arg Ala Asn Ala Ala Leu Thr Pro Glu Gln Arg Asp Trp Thr			
320	325	330	
ttt gac ttg tta acg ggt cag gga gct tat tct gct gat cag aca aac			1719
Phe Asp Leu Leu Thr Gly Gln Gly Ala Tyr Ser Ala Asp Gln Thr Asn			
335	340	345	350
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Tyr His Trp Gly Ala Tyr Ala Gln Ile Ser Ser Thr Ala Ile Arg Ala			
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tgg aag gcg ctc tct cga gca ggt gaa acc act ggt cag tta aca aaa			1815
Trp Lys Ala Leu Ser Arg Ala Gly Glu Thr Thr Gly Gln Leu Thr Lys			
370	375	380	
ata atc cag gga cct cag gaa tct ttc tca gat ttt gtg gcc aga atg			1863
Ile Ile Gln Gly Pro Gln Glu Ser Phe Ser Asp Phe Val Ala Arg Met			
385	390	395	
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Thr Glu Ala Ala Glu Arg Ile Phe Gly Glu Ser Glu Gln Ala Ala Pro			
400	405	410	
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Leu Ile Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala			
415	420	425	430
gcc ata gcc cca aga aag aac aaa ggc tta caa gac tgg ctc agg gtc			2007
Ala Ile Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val			
435	440	445	
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Cys	Arg	Glu	Leu	Gly	Gly	Pro	Leu	Ser	Asn	Ala	Gly	Leu	Ala	Ala	Ala	
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atc	ctt	caa	tcc	caa	aac	cgc	tcc	atg	ggc	aga	aat	gat	cag	agg	aca	2103
Ile	Leu	Gln	Ser	Gln	Asn	Arg	Ser	Met	Gly	Arg	Asn	Asp	Gln	Arg	Thr	
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																470
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tgt	ttt	aac	tgc	gga	aag	cct	ggg	cat	ttt	aag	aaa	gat	tgc	aga	gct	2151
Cys	Phe	Asn	Cys	Gly	Lys	Pro	Gly	His	Phe	Lys	Lys	Asp	Cys	Arg	Ala	
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cca	gat	aaa	cag	gga	ggg	act	ctc	act	ctt	tgc	tct	aag	tgt	ggc	aag	2199
Pro	Asp	Lys	Gln	Gly	Gly	Thr	Leu	Thr	Leu	Cys	Ser	Lys	Cys	Gly	Lys	
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Gly	Tyr	His	Arg	Ala	Asp	Gln	Cys	Arg	Ser	Val	Arg	Asp	Ile	Lys	Gly	
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aga	att	ctt	ccc	cca	cct	gat	agt	caa	tca	gct	gat	gtg	cca	aaa	aac	2295
Arg	Ile	Leu	Pro	Pro	Pro	Asp	Ser	Gln	Ser	Ala	Asp	Val	Pro	Lys	Asn	
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Phe	Val	Arg	Thr	Gln	Glu	Ala	Val	Arg	Glu	Thr	Thr	Gln	Glu	Asp	Pro	
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																570
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Met	Ser	Ile	Gln	Pro	Val	Pro	Val	Glu	Pro	Ile	Pro	Ser	Leu	Pro	Pro	
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																600
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Gly	Thr	Met	Gly	Leu	Ile	Leu	Gly	Arg	Gly	Ser	Leu	Thr	Leu	Gln	Gly	
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																620
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Leu	Val	Val	His	Pro	Gly	Ile	Met	Asp	Cys	Gln	His	Ser	Pro	Glu	Ile	
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cag	gtc	ctg	tgc	tca	agc	cct	aaa	ggc	gtt	ttt	tct	att	agt	aaa	gga	2630
Gln	Val	Leu	Cys	Ser	Ser	Pro	Lys	Gly	Val	Phe	Ser	Ile	Ser	Lys	Gly	
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gat	agg	ata	gct	cag	ctg	ctg	ctc	cct	gat	aat	acc	agg	gag	aaa	2678	
Asp	Arg	Ile	Ala	Gln	Leu	Leu	Leu	Leu	Pro	Asp	Asn	Thr	Arg	Glu	Lys	
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																665
tct	gca	gga	cct	gag	ata	aag	aaa	atg	ggc	tcc	tca	gga	aat	gat	tct	2726
Ser	Ala	Gly	Pro	Glu	Ile	Lys	Lys	Met	Gly	Ser	Ser	Gly	Asn	Asp	Ser	

670	675	680	685		
gcc tat ttg gtt gta tct tta aat gat aga cct aag ctc cgc ctt aag Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu Arg Leu Lys	690	695	700	2774	
att aat gga aaa gag ttt gaa ggc atc ctt gat acc gga gca gat aaa Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly Ala Asp Lys	705	710	715	2822	
agt ata att tct aca cat tgg tgg ccc aaa gca tgg ccc acc aca gag Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro Thr Thr Glu	720	725	730	2870	
tca tct cat tca tta cag ggc cta gga tat caa tca tgt ccc act ata Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys Pro Thr Ile	735	740	745	2918	
agc tcc gtt gcc ttg acg tgg gaa tcc tct gaa ggg cag caa ggg aaa Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln Gln Gly Lys	750	755	760	765	2966
ttc ata cct tat gtg ctc cca ctc ccg gtt aac ctc tgg gga agg gat Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp Gly Arg Asp	770	775	780	3014	
att atg cag cat ttg ggc ctt att ttg tcc aat gaa aac gcc cca tca Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn Ala Pro Ser	785	790	795	3062	
gga ggg tat tca gct aaa gca aaa aat atc atg gca aag atg ggt tat Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys Met Gly Tyr	800	805	810	3110	
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taaaattagg ccatattgaa ccctctacct caccttggaa tactccaatt tttgttaatta agaaaaagtc aggaaagtgg agactgctcc atgacacctag agccatataat gagcaa atg	860	865	870	3323	
aac tta ttt ggc cca gta cag agg ggt ctc cct gta ctt tcc gcc tta Asn Leu Phe Gly Pro Val Gln Arg Gly Leu Pro Val Leu Ser Ala Leu	875	880	885	3383	
cca cgt ggc tgg aat tta atc att ata gat att aaa gat tgt ttc ttt Pro Arg Gly Trp Asn Leu Ile Ile Asp Ile Lys Asp Cys Phe Phe	890	895	900	3442	
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				845	
				3490	
				3538	

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Ser Ile Pro Leu Cys Pro Arg Asp Arg Pro Arg Phe Ala Phe Thr Ile			
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ccc tct att aat cac atg gaa cct gat aag agg tat caa tgg aag gtc			3634
Pro Ser Ile Asn His Met Glu Pro Asp Lys Arg Tyr Gln Trp Lys Val			
895	900	905	
tta cca cag gga atg tcc aat agt cct act atg tgt caa ctt tat gta			3682
Leu Pro Gln Gly Met Ser Asn Ser Pro Thr Met Cys Gln Leu Tyr Val			
910	915	920	925
caa gaa gct ctt ttg cca gtg agg gaa caa ttc ccc tct tta att ttg			3730
Gln Glu Ala Leu Leu Pro Val Arg Glu Gln Phe Pro Ser Leu Ile Leu			
930	935	940	
ctc ctt tac atg gat gac atc ctc ctg tgc cat aaa gac ctt acc atg			3778
Leu Leu Tyr Met Asp Asp Ile Leu Leu Cys His Lys Asp Leu Thr Met			
945	950	955	
cta caa aag gca tat cct ttt cta ctt aaa act tta agt cag tgg ggt			3826
Leu Gln Lys Ala Tyr Pro Phe Leu Leu Lys Thr Leu Ser Gln Trp Gly			
960	965	970	
cta cag ata gcc aca gaa aag gtc caa att tct gat aca gga caa ttc			3874
Leu Gln Ile Ala Thr Glu Lys Val Gln Ile Ser Asp Thr Gly Gln Phe			
975	980	985	
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Leu Gly Ser Val Val Ser Pro Asp Lys Ile Val Pro Gln Lys Val Glu			
990	995	1000	1005
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Ile Arg Arg Asp His Leu His Thr Leu Asn Asp Phe Gln Lys Leu			
1010	1015	1020	
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Leu Gly Asp Ile Asn Trp Leu Arg Pro Phe Leu Lys Ile Pro Ser			
1025	1030	1035	
gct gaa tta agg cct ttg ttt agt att tta gaa gga gat cct cat			4057
Ala Glu Leu Arg Pro Leu Phe Ser Ile Leu Glu Gly Asp Pro His			
1040	1045	1050	
atc tcc tcc cct agg act ctt act cta gct gct aac cag gcc tta			4102
Ile Ser Ser Pro Arg Thr Leu Thr Leu Ala Ala Asn Gln Ala Leu			
1055	1060	1065	
caa aaa gtg gaa aaa gcc tta cag aat gca caa tta caa cgt att			4147
Gln Lys Val Glu Lys Ala Leu Gln Asn Ala Gln Leu Gln Arg Ile			
1070	1075	1080	
gag gat tcg cag cct ttc agt ttg tgt gtc ttt aag aca gca caa			4192
Glu Asp Ser Gln Pro Phe Ser Leu Cys Val Phe Lys Thr Ala Gln			
1085	1090	1095	
ttg cca act gca gtt ttg tgg cag aat ggg cca ttg ttg tgg atc			4237

Leu Pro Thr Ala Val Leu Trp Gln Asn Gly Pro Leu Leu Trp Ile
1100 1105 1110

cat cca aac gta tcc cca gct aaa ata ata gat tgg tat cct gat 4282
His Pro Asn Val Ser Pro Ala Lys Ile Ile Asp Trp Tyr Pro Asp
1115 1120